

Please substitute the following claim set for the pending claim set.

1-89. (Cancelled)

90. (Currently amended) A method of karyotyping a genome of a test eukaryotic cell, comprising:

identifying pieces of the genome of the test eukaryotic cell by determining nucleotide sequence of said pieces;

enumerating the pieces within a plurality of windows of fixed size of the genome, each of said windows having the fixed size, wherein each window comprises a plurality of pieces and the pieces within a window are genomically clustered;

performing a plurality of comparisons for the plurality of windows in which a first number of pieces enumerated within a window for the test eukaryotic cell is compared to a second number of pieces enumerated within the window for a reference eukaryotic cell, wherein a difference between the first number and the second number indicates a karyotypic difference between the test eukaryotic cell and the reference eukaryotic cell.

91. (Canceled)

92. (Currently amended) The method of claim 90 wherein the pieces within ~~the~~ each window map within 40 kb.

93. (Currently amended) The method of claim 90 wherein the pieces within ~~the~~ each window map within 200 kb.

94. (Currently amended) The method of claim 90 wherein the pieces within ~~the~~ each window map within 600 kb.

95. (Currently amended) The method of claim 90 wherein the pieces within ~~the~~ each window map within 4 Mb.

96. (Currently amended) The method of claim 90 wherein the ~~piece is~~ pieces are defined by the presence of a Bcgl restriction endonuclease recognition site which is flanked by 12 nucleotides on either end.

97. (Previously Presented) The method of claim 90 further comprising the step of:
identifying aneuploidy if (a) pieces of one or more autosomes are determined to be present in the test eukaryotic cell relative to the reference eukaryotic cell at a ratio of 1.5 or greater or less than 0.7; or (b) pieces of one or more sex chromosomes in a male are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 1.5 or greater or less than 0.7; or (c) pieces of X chromosomes in a female are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 3 or greater or less than 1.5 or relative to a reference female eukaryotic cell at a ratio of 1.5 or greater or less than 0.7.

98. (Previously Presented) The method of claim 90 wherein pieces representing less than 15 % of the genome of the eukaryotic cell are enumerated in the step of enumerating.

99. (Currently amended) A method of determining changes in copy number of portions of the genome of a test eukaryotic cell, comprising:

identifying pieces of the genome of the test eukaryotic cell by determining nucleotide sequence of said pieces;

enumerating the pieces within a plurality of windows of fixed size of the genome, each of said windows having the fixed size, wherein each window comprises a plurality of pieces and the pieces within a window are genomically clustered;

performing a plurality of comparisons for the plurality of windows in which a first number of pieces enumerated within a window for the test eukaryotic cell is compared to a second number of pieces enumerated within the window for a reference eukaryotic cell, wherein a difference between the first number and the second number indicates a change in copy number of a portion of the genome between the test eukaryotic cell and the reference eukaryotic cell.

100. (Previously Presented) The method of claim 99 wherein the change in copy number is due to gain or loss of a whole chromosome.

101. (Previously Presented) The method of claim 99 wherein the change in copy number is due to a gain or loss of a chromosomal arm.

102. (Previously Presented) The method of claim 99 wherein the change in copy number is due to an interstitial amplification.

103. (Previously Presented) The method of claim 99 wherein the change in copy number is due to an interstitial deletion.

104. (Currently amended) The method of claim 99 wherein the pieces within ~~the~~ each window map within 40 kb.

105. (Currently amended) The method of claim 99 wherein the pieces within ~~the~~ each window map within 200 kb.

106. (Currently amended) The method of claim 99 wherein the pieces within ~~the~~ each window map within 600 kb.

107. (Currently amended) The method of claim 99 wherein the pieces within ~~the~~ each window map within 4 Mb.

108. (Currently amended) The method of claim 99 wherein the ~~piece is~~ pieces are defined by the presence of a Bcgl restriction endonuclease recognition site which is flanked by 12 nucleotides on either end.

109. (Previously Presented) The method of claim 99 further comprising the step of:
identifying aneuploidy if (a) pieces of one or more autosomes are determined to be present in the test eukaryotic cell relative to the reference eukaryotic cell at a ratio of 1.5 or greater or less than 0.7; or (b) pieces of one or more sex chromosomes in a male are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 1.5 or greater or less than 0.7; or (c) pieces of X chromosomes in a female are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 3 or greater or less than 1.5 or relative to a reference female eukaryotic cell at a ratio of 1.5 or greater or less than 0.7.

110. (Previously Presented) The method of claim 99 wherein pieces representing less than 15 % of the genome of the eukaryotic cell are enumerated in the step of enumerating.